

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Jeffrey E. Russell Examiner #: 62785 Date: 2-3-2005  
 An Unit: 1654 Phone Number: 571-272-0969 Serial Number: 101705, 857  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL  
REN 3C18 (mailbox), 3D19 (office)

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of invention: Effect on Calcium Channels To Prevent or Treat Wrinkles and Fine Lines

Inventors (please provide full names): B. Renault

Earliest Priority Filing Date: 11-13-2003

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO:2 (EEMQRR) in STN, in the US patent application sequence database (pending, published, + issued), and in Genoseq/Swissprot/PIR.

Thank you.

JER

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep. / Review Time _____	Fulltext _____	Sequence Systems _____
Clerical Prep. Time: _____	Patent Family _____	WWW/Internet _____
On line Time _____	Other _____	Other (specify) _____

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 5, 2005, 22:35:25 ; Search time 163 Seconds  
(without alignments)  
14.237 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 EMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	6	4	AAB15582 Human SNA
2	30	100.0	6	8	ADP13167 SNAP 25 p
3	30	100.0	13	4	AAB15583 Human SNA
4	30	100.0	13	8	ADP13168 SNAP 25 p
5	30	100.0	64	3	AAG00764 Human sec
6	30	100.0	82	4	AAB15581 Human SNA
7	30	100.0	82	8	ADP13166 SNAP 25 p
8	30	100.0	93	6	ABU43453 Protein e
9	30	100.0	106	3	AAG03825 Human sec
10	30	100.0	106	3	AAG03826 Human sec
11	30	100.0	198	4	AAU00255 Synapto
12	30	100.0	199	4	AAU00263 Synapto
13	30	100.0	200	4	AAU00264 Synapto
14	30	100.0	200	8	ADN11044 Murine SN
15	30	100.0	201	4	AAU02637 Synapto
16	30	100.0	202	4	AAU00265 Synapto
17	30	100.0	203	4	AAU02636 Synapto
18	30	100.0	206	2	AAW30103 Synapto
19	30	100.0	206	2	AAW43426 Mouse syn
20	30	100.0	206	2	AAW79198 Mouse syn
21	30	100.0	206	4	AAU00256 Synapto
22	30	100.0	206	4	AAU00261 Synapto
23	30	100.0	206	4	AAU00246 Synapto
24	30	100.0	206	4	AAU00253 SNARE hom
25	30	100.0	206	4	AAU02171 Synapto

ALIGNMENTS

RESULT 1

AAB15582

ID AAB15582 standard; peptide; 6 AA.

XX AC AAB15582;

XX DT 02-MAR-2001 (first entry)

XX DE Human SNAP-25 N-terminal peptide #2.

XX KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator; SNAP-25; synaptoosomal-associated protein 25; facial wrinkle; asymmetry; neurodegenerative disorder.

XX OS Homo sapiens.

XX PN WO200064932-A1.

XX PD 02-NOV-2000.

XX PF 18-FEB-2000; 2000WO-ES000058.

XX PR 23-APR-1999; 99ES-00000844.

XX (LIPO-) LIPOTEC SA.

XX Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI; Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV; Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T; Perez Paya E;

XX WPI; 2001-007091/01.

XX New peptides containing amino acid sequences from known proteins for treatment of neurological disorders.

XX Claim 9; Page 32; 40pp; Spanish.

XX The invention relates to new peptides comprising 3-30 contiguous amino acids from the N-terminus of the protein SNAP-25 (synaptoosomal-associated protein 25). The peptides AAB15581-B15586 represent examples of the peptides of the invention. The peptides have neuronal exocytosis inhibitory activity and are used for treatment of facial wrinkles and asymmetry and pathological neuronal exocytosis-mediated pathological disorders and alterations manifested e.g. by spasms and neurological and neurodegenerative disorders

XX Sequence 6 AA;

Query Match  
Best Local Similarity 100.0%; Score 30; DB 4; Length 6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
DB 1 EEMQRR 6

RESULT 2  
ID ADP13167 standard; peptide; 6 AA.  
XX ADP13167;  
AC ADP13167;  
XX 29-JUL-2004 (first entry)  
XX SNAP 25 protein N-terminal domain peptide fragment, SEQ ID 2.  
DE Dermatological; Synaptosomal Associated Protein 25kDa; SNAP 25;  
KW anti-wrinkle.  
XX Unidentified.  
OS FR2846885-A1.  
XX 14-MAY-2004.  
XX 13-NOV-2002; 2002FR-00014183.  
XX 13-NOV-2002; 2002FR-00014183.  
XX (OREA ) L'OREAL SA.  
XX Renault B;  
PI WPI; 2004-402925/38.  
XX Topical cosmetic composition for smoothing skin wrinkles and fine lines  
PT containing synergistic combination of peptide with sequence based on SNAP  
PT 25 protein and calcium channel inhibitor.  
XX Claim 4; SEQ ID NO 2; 23pp; French.

CC The present invention relates to novel compositions (A) for topical  
CC application to the skin. (A) comprises physiological medium containing at  
CC least one Synaptosomal Associated Protein 25kDa (SNAP 25) peptide (I);  
CC ADP13166-ADP13171) and at least one calcium channel inhibitor (II). The  
CC combination of (I) and (II) has a synergistic effect in combating  
CC wrinkles. As well as their known anti-wrinkle activity based on SNAP  
CC receptor complex inhibition, (II) have been found to show synergistic  
CC effect in antagonizing type I calcium channels when used in combination  
CC with (II) which are also known anti-wrinkle agents. (A) are used  
CC cosmetically as topically applied agents for treating and/or preventing  
CC (specifically smoothing) wrinkles and fine lines, especially expression  
CC wrinkles by application to the face or forehead, particularly by  
CC application to wrinkles and fine lines located radially around the mouth  
CC and/or eyes, horizontally on the forehead or in the space between the  
CC eyebrows.

XX Sequence 6 AA;  
QY 1 EEMQRR 6  
DB 1 EEMQRR 6

Query Match  
Best Local Similarity 100.0%; Score 30; DB 8; Length 6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
DB 1 EEMQRR 6

RESULT 3  
ID ADP13168 standard; peptide; 13 AA.  
XX ADP13168;  
AC ADP13168;  
XX 29-JUL-2004 (first entry)  
XX SNAP 25 protein N-terminal domain peptide fragment, SEQ ID 3.  
DE Dermatological; Synaptosomal Associated Protein 25kDa; SNAP 25;  
KW anti-wrinkle.  
XX Unidentified.  
OS FR2846885-A1.  
XX

XX PD 14-MAY-2004.  
 XX XX  
 XX PF 13-NOV-2002; 2002FR-00014183.  
 XX XX  
 XX PF 13-NOV-2002; 2002FR-00014183.  
 XX XX  
 XX PA (OREA ) L'OREAL SA.  
 XX XX  
 XX PI Renault B;  
 XX XX  
 XX DR WPI; 2004-402925/38.  
 XX XX  
 XX PT Topical cosmetic composition for smoothing skin wrinkles and fine lines  
 XX PT containing synergistic combination of peptide with sequence based on SNAP  
 XX PT 25 protein and calcium channel inhibitor.  
 XX XX  
 XX PS Claim 4; SEQ ID NO 3; 23pp; French.  
 XX XX  
 XX CC The present invention relates to novel compositions (A) for topical  
 XX CC application to the skin. (A) comprises physiological medium containing at  
 XX CC least one Synaptosomal Associated Protein 25kDa (SNAP 25) peptide (I;  
 XX CC ADP13166-ADP13171) and at least one calcium channel inhibitor (II). The  
 XX CC combination of (I) and (II) has a synergistic effect in combating  
 XX CC wrinkles. As well as their known anti-wrinkle activity based on SNAP  
 XX CC receptor complex inhibition, (I) have been found to show synergistic  
 XX CC effect in antagonizing type L calcium channels when used in combination  
 XX CC with (II) which are also known anti-wrinkle agents. (A) are used  
 XX CC cosmetically as topically applied agents for treating and/or preventing  
 XX CC (specifically smoothing) wrinkles and fine lines, especially expression  
 XX CC wrinkles by application to the face or forehead, particularly by  
 XX CC application to wrinkles and fine lines located radially around the mouth  
 XX CC and/or eyes, horizontally on the forehead or in the space between the  
 XX CC eyebrows.  
 XX XX  
 XX SQ Sequence 13 AA;  
 XX  
 XX Query Match 100.0%; Score 30; DB 8; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 21;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 EEMQRR 6  
 XX DB |||||  
 XX 3 EEMQRR 8  
 XX  
 XX RESULT 5  
 XX AAG00764  
 XX ID AAG00764 standard; protein; 64 AA.  
 XX AC  
 XX XX AAG00764;  
 XX DT 06-OCT-2000 (first entry)  
 XX XX  
 XX DE Human secreted protein, SEQ ID NO: 4845.  
 XX XX  
 XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 XX KW gene therapy; chromosome mapping.  
 XX XX  
 XX OS Homo sapiens.  
 XX XX  
 XX PN EP1033401-A2.  
 XX XX  
 XX PD 06-SEP-2000.  
 XX XX  
 XX PF 21-FEB-2000; 2000EP-00200610.  
 XX XX  
 XX PR 26-FEB-1999; 99US-0122487P.  
 XX XX  
 XX PA (GEST ) GENSET.  
 XX XX  
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX XX

DR WPI; 2000-500381/45.  
 DR N-PSDB; AAC00770.  
 XX  
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 XX XX  
 XX PS Claim 13; SEQ ID NO 4845; 71pp + Sequence Listing; English.  
 XX XX  
 XX CC The present sequence is a polypeptide encoded by one of a large number of  
 XX CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
 XX CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
 XX CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
 XX CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
 XX CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
 XX CC sequences derived from the 5' ends of mRNAs and even in those cases where  
 XX CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
 XX CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
 XX CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
 XX CC are also used in diagnostic, forensic, gene therapy and chromosome  
 XX CC mapping procedures. They are used to obtain upstream regulatory sequences  
 XX CC and to design expression and secretion vectors  
 XX XX  
 XX SQ Sequence 64 AA;  
 XX  
 XX Query Match 100.0%; Score 30; DB 3; Length 64;  
 XX Best Local Similarity 100.0%; Pred. No. 96;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 EEMQRR 6  
 XX DB |||||  
 XX 12 EEMQRR 17  
 XX  
 XX RESULT 6  
 XX AAB15581  
 XX ID AAB15581 standard; peptide; 82 AA.  
 XX AC  
 XX XX AAB15581;  
 XX DT 02-MAR-2001 (first entry)  
 XX XX  
 XX DE Human SNAP-25 N-terminal peptide #1.  
 XX XX  
 XX KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;  
 XX KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;  
 XX KW neurodegenerative disorder.  
 XX XX  
 XX OS Homo sapiens.  
 XX XX  
 XX PN WO200064932-A1.  
 XX XX  
 XX PD 02-NOV-2000.  
 XX XX  
 XX PF 18-FEB-2000; 2000WO-ES000058.  
 XX XX  
 XX PR 23-APR-1999; 99ES-00000844.  
 XX XX  
 XX PA (LIPO-) LIPOTEC SA.  
 XX XX  
 XX PI Planes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;  
 XX PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;  
 XX PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;  
 XX PI Perez Paya E;  
 XX XX  
 XX DR WPI; 2001-007091/01.  
 XX XX  
 XX PT New peptides containing amino acid sequences from known proteins for  
 XX PT treatment of neurological disorders.  
 XX XX  
 XX PS Claim 1; Page 31; 40pp; Spanish.  
 XX XX  
 XX CC The invention relates to new peptides comprising 3-30 contiguous amino

CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated  
CC protein 25). The peptides AAI5581-B15586 represent examples of the  
CC peptides of the invention. The peptides have neuronal exocytosis  
CC inhibitory activity and are used for treatment of facial wrinkles and  
CC asymmetry and pathological neuronal exocytosis-mediated pathological  
CC disorders and alterations manifested e.g. by spasms and neurological and  
CC neurodegenerative disorders

XX SQ Sequence 82 AA;

Query Match 100.0%; Score 30; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
| | | | |  
DB 11 EEMQRR 16

RESULT 7  
ADP13166  
ID ADP13166 standard; protein; 82 AA.

XX AC ADP13166;

DT 29-JUL-2004 (first entry)

XX DE SNAP 25 protein N-terminal domain protein, SEQ ID 1.

XX KW Dermatological; Synaptosomal Associated Protein 25kDa; SNAP 25;  
XX KW anti-wrinkle.

XX OS Unidentified.

XX PN FR2846885-A1.

XX PD 14-MAY-2004.

XX PF 13-NOV-2002; 2002FR-00014183.

XX PR 13-NOV-2002; 2002FR-00014183.

XX PA (OREA ) L'OREAL SA.

XX PI Renault B;

XX PS WPI; 2004-402925/38.

XX CC Topical cosmetic composition for smoothing skin wrinkles and fine lines  
XX CC containing synergistic combination of peptide with sequence based on SNAP  
XX CC 25 protein and calcium channel inhibitor.

XX CC Claim 4; SEQ ID NO 1; 23pp; French.

XX CC The present invention relates to novel compositions (A) for topical  
XX CC application to the skin. (A) comprises physiological medium containing at  
XX CC least one Synaptosomal Associated Protein 25kDa (SNAP 25) peptide (I);  
XX CC ADP13166-ADP13171) and at least one calcium channel inhibitor (II). The  
XX CC combination of (I) and (II) has a synergistic effect in combating  
XX CC wrinkles. As well as their known anti-wrinkle activity based on SNAP  
XX CC receptor complex inhibition, (I) have been found to show synergistic  
XX CC effect in antagonizing type L calcium channels when used in combination  
XX CC with (II) which are also known anti-wrinkle agents. (A) are used  
XX CC cosmetically as topically applied agents for treating and/or preventing  
XX CC (specifically smoothing) wrinkles and fine lines, especially by  
XX CC wrinkles by application to the face or forehead, particularly by  
XX CC application to wrinkles and fine lines located radially around the mouth  
XX CC and/or eyes, horizontally on the forehead or in the space between the  
XX CC eyebrows.

XX SQ Sequence 82 AA;

Query Match 100.0%; Score 30; DB 8; Length 82;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
| | | | |  
DB 11 EEMQRR 16

RESULT 8  
ABU43453  
ID ABU43453 standard; protein; 93 AA.

XX AC ABU43453;

DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #28980.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Staphylococcus haemolyticus.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zvakind JW;  
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA47323.

XX PT New antisense nucleic acids, useful for identifying proteins or screening  
XX PT for homologous nucleic acids required for cellular proliferation to  
XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 71377; 1765pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of  
XX CC the 6213 antisense sequences given in the specification where expression  
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid  
XX CC encoding a polypeptide whose expression is inhibited by the antisense  
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX CC polypeptide or its fragment whose expression is inhibited by the  
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding  
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX CC proliferation or the activity of a gene in an operon required for  
XX CC proliferation; (7) identifying a compound that influences the activity of  
XX CC the gene product or that has an activity against a biological pathway  
XX CC required for proliferation, or that inhibits cellular proliferation; (8)  
XX CC identifying a gene required for cellular proliferation or the biological  
XX CC pathway in which a proliferation-required gene or its gene product lies  
XX CC or a gene on which the test compound that inhibits proliferation of an  
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX CC compound's activity; (11) a culture comprising strains in which the gene  
XX CC product is overexpressed or underexpressed; (12) determining the extent  
XX CC to which each of the strains is present in a culture or collection of  
XX CC strains; or (13) identifying the target of a compound that inhibits the  
XX CC proliferation of an organism. The antisense nucleic acids are useful for  
XX CC identifying proteins or screening for homologous nucleic acids required  
XX CC for cellular proliferation to isolate candidate molecules for rational  
XX CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
XX

SQ Sequence 93 AA;

Query Match 100.0%; Score 30; DB 6; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||||  
DB 24 EEMQRR 29

RESULT 9

AAAG03825  
ID AAAG03825 standard; protein; 106 AA.

AC AAAG03825;

XX 06-OCT-2000 (first entry)

DT Human secreted protein, SEQ ID NO: 7906.

DE Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

PN 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST ) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.

DR N-PSDB; AAC03831.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 7906; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors

SQ Sequence 106 AA;

Query Match 100.0%; Score 30; DB 3; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||||  
DB 12 EEMQRR 17

RESULT 10

AAAG03826  
ID AAAG03826 standard; protein; 106 AA.

XX AAAG03826;

XX 06-OCT-2000 (first entry)

DT Human secreted protein, SEQ ID NO: 7907.

DE Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

PN 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST ) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.

DR N-PSDB; AAC03832.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 7907; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors

SQ Sequence 106 AA;

Query Match 100.0%; Score 30; DB 3; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||||  
DB 12 EEMQRR 17

RESULT 11

AAU00255  
ID AAU00255 standard; protein; 198 AA.

XX AAU00255;

XX

DT 12-SEP-2001 (first entry)  
 XX Synaptosomal-associated protein, SNAP25, C-terminal deletion 1-198.  
 DE SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KW synaptosomal-associated protein; mouse; mutant; mutein;  
 KW N-ethylmaleimide-sensitive fusion protein;  
 KW soluble NSF-attachment protein receptor.  
 XX Mus sp.  
 OS Synthetic.  
 XX WO200118038-A2.  
 XX 15-MAR-2001.  
 XX 18-AUG-2000; 2000WO-GB003196.  
 XX 20-AUG-1999; 99US-0149993P.  
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
 XX WPI; 2001-226739/23.  
 XX Treating a patient suffering from poisoning or at risk of poisoning by a  
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
 PT resistant or toxin-inhibitory SNARE.  
 XX Example 1; Page; 131pp; English.  
 XX The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, C-terminal deletion 1-198, used in a new  
 CC method of treating a patient suffering from poisoning or at risk of  
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)  
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
 CC useful in the manufacture of a medicament for the treatment of a patient  
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
 CC polynucleotide encoding either of these SNARE polypeptides are useful in  
 CC the manufacture of medicament for the treatment of a patient in need of  
 CC inhibition of SNARE-dependent exocytosis from a cell capable of  
 CC performing SNARE-dependent exocytosis. The method of treatment is  
 CC relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state. Note: The present sequence is  
 CC not shown in the specification but is derived from the mouse SNAP-25  
 CC sequence given in figure 8 (see AAU00246)  
 XX Sequence 199 AA;  
 SQ Query Match 100.0%; Score 30; DB 4; Length 198;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EEMQRR 6  
 Db 12 EEMQRR 17  
 RESULT 12  
 AAU00263  
 ID AAU00263 standard; protein; 199 AA.

XX AAU00263;  
 XX 12-SEP-2001 (first entry)  
 XX Synaptosomal-associated protein, SNAP25, mutant 1-199 (R198T).  
 DE SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KW synaptosomal-associated protein; mouse; mutant; mutein;  
 KW N-ethylmaleimide-sensitive fusion protein;  
 KW soluble NSF-attachment protein receptor.  
 XX Mus sp.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"  
 XX WO200118038-A2.  
 XX 15-MAR-2001.  
 XX 18-AUG-2000; 2000WO-GB003196.  
 XX 20-AUG-1999; 99US-0149993P.  
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
 XX WPI; 2001-226739/23.  
 XX Treating a patient suffering from poisoning or at risk of poisoning by a  
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
 PT resistant or toxin-inhibitory SNARE.  
 XX Example 1; Page; 131pp; English.  
 XX The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant 1-199 (R198T), used in a new method of  
 CC treating a patient suffering from poisoning or at risk of poisoning by a  
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-  
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to  
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the  
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin  
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating  
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell  
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a  
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE  
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE  
 CC or a recombinant polynucleotide encoding the SNARE is useful in the  
 CC manufacture of a medicament for the treatment of a patient suffering from  
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from  
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a  
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding  
 CC either of these SNARE polypeptides are useful in the manufacture of  
 CC medicament for the treatment of a patient in need of inhibition of SNARE-  
 CC dependent exocytosis from a cell capable of performing SNARE-dependent  
 CC exocytosis. The method of treatment is relatively fast, thus alleviating  
 CC the symptoms when most severe and taking the patient out of critical  
 CC state. Note: The present sequence is not shown in the specification but  
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see  
 CC AAU00246)  
 XX Sequence 199 AA;  
 SQ Query Match 100.0%; Score 30; DB 4; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EEMQRR 6



Db 12 EEMQRR 17

RESULT 13  
AAU00264

XX AAU00264 standard; protein; 200 AA.  
AC  
XX  
XX  
XX 12-SEP-2001 (first entry)  
XX  
XX Synaptosomal-associated protein, SNAP25, mutant 1-200 (R198T).  
XX  
XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
KW synaptosomal-associated protein; mouse; mutant; mutein;  
KW N-ethylmaleimide-sensitive fusion protein;  
KW soluble NSF-attachment protein receptor.  
XX  
XX Mus sp.  
OS  
OS Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"  
FT  
XX  
XX WO200118038-A2.  
XX  
XX 15-MAR-2001.  
XX  
XX 18-AUG-2000; 2000WO-GB003196.  
XX  
XX 20-AUG-1999; 99US-0149993P.  
XX  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
XX WPI; 2001-226739/23.  
XX  
XX Treating a patient suffering from poisoning or at risk of poisoning by a  
PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
PT resistant or toxin-inhibitory SNARE.  
XX  
XX Example 1; Page; 131pp; English.  
XX  
XX The sequence represents the amino acid sequence of synaptosomal-  
CC associated protein, SNAP25, mutant 1-200(R198T), used in a new method of  
CC treating a patient suffering from poisoning or at risk of poisoning by a  
CC clostridial toxin, comprising supplying a SNARE (soluble (N-  
CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to  
CC a cell of the patient, where the SNARE is resistant to proteolysis by the  
CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin  
CC (toxin-inhibitory SNARE). The protein can be used in a method of treating  
CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell  
CC capable of performing SNARE-dependent exocytosis, comprises supplying a  
CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE  
CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE  
CC or a recombinant polynucleotide encoding the SNARE is useful in the  
CC manufacture of a medicament for the treatment of a patient suffering from  
CC poisoning or at risk of poisoning by clostridial toxin, e.g. from  
CC botulism or tetanus. The fragment, variant, fusion or derivative of a  
CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding  
CC either of these SNARE polypeptides are useful in the manufacture of  
CC medicament for the treatment of a patient in need of inhibition of SNARE-  
CC dependent exocytosis from a cell capable of performing SNARE-dependent  
CC exocytosis. The method of treatment is relatively fast, thus alleviating  
CC the symptoms when most severe and taking the patient out of critical  
CC state. Note: The present sequence is not shown in the specification but  
CC is derived from the mouse SNAP-25 sequence given in figure 8 (see  
XX AAU00246)

SQ Sequence 200 AA;  
Query Match 100.0%; Score 30; DB 4; Length 200;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
DB 12 EEMQRR 17

RESULT 14  
ADN11044

XX ADN11044 standard; protein; 200 AA.  
XX  
XX ADN11044;  
XX  
XX 01-JUL-2004 (first entry)  
XX  
XX Murine SNAP-25, substrate of botulinum toxin.  
XX  
XX Neurotoxin; BoNT; botulism; antidote; mouse; SNAP-25.  
XX  
XX Mus musculus.  
OS  
OS Synthetic.  
XX  
XX WO2004031355-A2.  
XX  
XX 15-APR-2004.  
XX  
XX 01-OCT-2003; 2003WO-US030899.  
XX  
XX 01-OCT-2002; 2002US-0415177P.  
XX  
XX (UYMA-) UNIV. MARYLAND BALTIMORE.  
XX  
XX Oyler GA, Tsai YC, Fishman PS, Kincaid RL;  
XX WPI; 2004-347972/32.  
XX N-PSDB; ADN11043.  
XX  
XX New botulinum neurotoxin substrate complex comprising a peptide  
PT substrate, a reporter domain, and an immobilization domain, useful for  
PT cell-based screening to monitor the catalytic activity of BoNT in living  
PT cells.  
XX  
XX Claim 23; SEQ ID NO 16; 85pp; English.  
XX  
XX The present sequence is the protein sequence of murine SNAP-25, a  
CC substrate of botulinum neurotoxin (BoNT). The invention provides a method  
CC for screening candidate inhibitors of BoNT for use in vitro and in living  
CC cells. Such a method can be used to accelerate the search for a  
CC clinically useful antidote to botulism. The method can be adapted for use  
CC as a high throughput screening assay. It uses a BoNT substrate complex  
CC composed of a peptide substrate that is cleaved at a specific site by a  
CC BoNT and which is flanked on one side by a reporter domain and on the  
CC other side by an immobilisation domain. The inhibitor is identified by  
CC its ability to decrease the relative amount of cleaved complex, detected  
CC through measuring a decrease in complex bound to a solid support.  
CC Preferred peptide substrates are SNAP-25, syntaxin and VAMP. Also  
CC provided are novel stable cells that express the BoNT substrate complex  
CC and viral vectors capable of efficiently expressing an active light chain  
CC of the BoNT within mammalian cells.  
XX  
XX SQ Sequence 200 AA;  
Query Match 100.0%; Score 30; DB 8; Length 200;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
DB 6 EEMQRR 11

RESULT 15  
AAU02637  
ID AAU02637 standard; protein; 201 AA.  
XX AC AAU02637;  
XX DT 12-SEP-2001 (first entry)  
XX DE Synaptosomal-associated protein, SNAP25, mutant 1-201(R198T).  
XX KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
KW synaptosomal-associated protein; mouse; mutant; mutein;  
KW N-ethylmaleimide-sensitive fusion protein;  
KW soluble NSF-attachment protein receptor.  
XX OS Mus SP.  
OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"  
FT XX WO200118038-A2.  
XX PN 15-MAR-2001.  
XX PD 18-AUG-2000; 2000WO-GB003196.  
XX PF 20-AUG-1999; 99US-0149993P.  
XX PR (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX PA Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
XX PI WPI; 2001-226739/23.  
XX DR  
XX PT Treating a patient suffering from poisoning or at risk of poisoning by a  
PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
PT resistant or toxin-inhibitory SNARE.  
XX  
XX Example 1; Page; 131pp; English.  
XX  
XX The sequence represents the amino acid sequence of synaptosomal-  
XX associated protein, SNAP25, mutant 1-201(R198T), used in a new method of  
XX treating a patient suffering from poisoning or at risk of poisoning by a  
XX clostridial toxin, comprising supplying a SNARE (soluble (N-  
XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to  
XX a cell of the patient, where the SNARE is resistant to proteolysis by the  
XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin  
XX (toxin-inhibitory SNARE). The protein can be used in a method of treating  
XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell  
XX capable of performing SNARE-dependent exocytosis, comprises supplying a  
XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE  
XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE  
XX or a recombinant polynucleotide encoding the SNARE is useful in the  
XX manufacture of a medicament for the treatment of a patient suffering from  
XX poisoning or at risk of poisoning by clostridial toxin, e.g. from  
XX botulism or tetanus. The fragment, variant, fusion or derivative of a  
XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding  
XX either of these SNARE polypeptides are useful in the manufacture of  
XX medicament for the treatment of a patient in need of inhibition of SNARE-  
XX dependent exocytosis from a cell capable of performing SNARE-dependent  
XX exocytosis. The method of treatment is relatively fast, thus alleviating  
XX the symptoms when most severe and taking the patient out of critical  
XX state. Note: The present sequence is not shown in the specification but  
XX is derived from the mouse SNAP-25 sequence given in figure 8 (see  
XX AAU00246)  
XX  
XX Sequence 201 AA;  
SQ

Query Match 100.0%; Score 30; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EEMQRR 6  
DB 12 EEMQRR 17  
Search completed: February 5, 2005, 23:12:03  
Job time : 164 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 5, 2005, 23:09:26 ; Search time 43 Seconds  
(without alignments)  
10.416 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	64	4	US-09-513-999C-4845
2	30	100.0	68	4	US-09-621-976-7614
3	30	100.0	106	4	US-09-513-999C-7906
4	30	100.0	106	4	US-09-513-999C-7907
5	30	100.0	159	4	US-09-902-540-13556
6	30	100.0	206	1	US-08-393-985-18
7	30	100.0	206	3	US-08-819-286-1
8	30	100.0	206	4	US-09-949-016-6311
9	30	100.0	219	4	US-09-949-016-10671
10	27	90.0	200	4	US-09-252-991A-23347
11	27	90.0	215	4	US-09-248-796A-19812
12	27	90.0	231	4	US-09-252-991A-27366
13	27	90.0	231	4	US-09-902-540-13879
14	27	90.0	314	4	US-09-543-681A-5695
15	27	90.0	375	1	US-07-803-622E-7
16	27	90.0	375	1	US-07-803-622E-9
17	27	90.0	376	4	US-09-270-767-42071
18	27	90.0	534	4	US-09-107-532A-6549
19	27	90.0	612	3	US-09-318-794A-5
20	27	90.0	739	1	US-07-803-622E-2
21	27	90.0	868	1	US-07-864-004B-6
22	27	90.0	868	1	US-08-251-937A-6
23	27	90.0	868	1	US-08-212-133A-3
24	27	90.0	914	3	US-09-437-054A-8
25	27	90.0	961	4	US-09-538-092-1231
26	27	90.0	1031	4	US-09-902-540-16773
27	27	90.0	1065	4	US-09-949-016-11618

28	27	90.0	1090	5	PCT-US93-03275-6	Sequence 6, Appli
29	27	90.0	2115	3	US-09-324-867-5	Sequence 5, Appli
30	27	90.0	2133	2	US-08-670-707A-37	Sequence 37, Appli
31	27	90.0	2133	3	US-09-037-601-37	Sequence 37, Appli
32	27	90.0	2133	3	US-09-315-179-37	Sequence 37, Appli
33	27	90.0	2133	4	US-09-523-656-30	Sequence 30, Appli
34	26	86.7	95	4	US-09-270-767-32716	Sequence 32716, A
35	26	86.7	120	4	US-09-809-920-6	Sequence 6, Appli
36	26	86.7	253	4	US-09-252-991A-31497	Sequence 31497, A
37	26	86.7	345	4	US-09-248-796A-20780	Sequence 20780, A
38	26	86.7	362	4	US-09-107-532A-7093	Sequence 7093, Ap
39	26	86.7	363	4	US-09-252-991A-32850	Sequence 32850, A
40	26	86.7	496	4	US-09-252-991A-20207	Sequence 20207, A
41	26	86.7	496	4	US-09-540-236-3821	Sequence 3821, Ap
42	26	86.7	631	4	US-09-949-016-11595	Sequence 11595, A
43	26	86.7	728	3	US-08-915-337-2	Sequence 2, Appli
44	26	86.7	745	4	US-09-549-016-9976	Sequence 9976, Ap
45	26	86.7	746	4	US-09-248-796A-20280	Sequence 20280, A

#### ALIGNMENTS

##### RESULT 1

US-09-513-999C-4845  
; Sequence 4845, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4845  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-4845

Query Match 100.0%; Score 30; DB 4; Length 64;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6  
Db 12 EEMQRR 17

##### RESULT 2

US-09-621-976-7614  
; Sequence 7614, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 7614  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-621-976-7614

Query Match 100.0%; Score 30; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
| | | | |  
DB 12 EEMQRR 17

## RESULT 3

US-09-513-999C-7906  
; Sequence 7906, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 7906  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 71  
; OTHER INFORMATION: Xaa=Met or Arg  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 72  
; OTHER INFORMATION: Xaa=Glu or Gly or Lys or Arg  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 92  
; OTHER INFORMATION: Xaa=Gly or Val  
; US-09-513-999C-7906

Query Match 100.0%; Score 30; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
| | | | |  
DB 12 EEMQRR 17

## RESULT 4

US-09-513-999C-7907  
; Sequence 7907, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 7907

LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 71  
; OTHER INFORMATION: Xaa=Met or Arg  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 72  
; OTHER INFORMATION: Xaa=Glu or Gly or Lys or Arg  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 92  
; OTHER INFORMATION: Xaa=Gly or Val  
; US-09-513-999C-7907

Query Match 100.0%; Score 30; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
| | | | |  
DB 12 EEMQRR 17

## RESULT 5

US-09-902-540-13556  
; Sequence 13556, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wisegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 13556  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
; US-09-902-540-13556

Query Match 100.0%; Score 30; DB 4; Length 159;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
| | | | |  
DB 147 EEMQRR 152

## RESULT 6

US-08-393-985-18  
; Sequence 18, Application US/08393985  
; Patent No. 5693476  
; GENERAL INFORMATION:  
; APPLICANT: Scheller, Richard H.  
; TITLE OF INVENTION: Methods and Compositions for Modulation  
; TITLE OF INVENTION: of Vesicular Release  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-393-985-18

Query Match 100.0%; Score 30; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 12 EEMQRR 17

RESULT 7
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-1

Query Match 100.0%; Score 30; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 12 EEMQRR 17

RESULT 8
US-09-949-016-6311
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6311

Query Match 100.0%; Score 30; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 12 EEMQRR 17

RESULT 9
US-09-949-016-10671
; Sequence 10671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10671
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10671

Query Match 100.0%; Score 30; DB 4; Length 219;
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Best Local Similarity 100.0%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
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Db 25 EEMQRR 30

RESULT 10  
US-09-252-991A-23347  
; Sequence 23347, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23347  
; LENGTH: 200  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23347

Query Match 90.0%; Score 27; DB 4; Length 200;  
Best Local Similarity 83.3%; Pred. No. 3.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
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Db 86 EELQRR 91

RESULT 11  
US-09-248-796A-19812  
; Sequence 19812, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 19812  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-19812

Query Match 90.0%; Score 27; DB 4; Length 215;  
Best Local Similarity 83.3%; Pred. No. 3.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||  
Db 98 EEMQRR 103

RESULT 12  
US-09-252-991A-27366  
; Sequence 27366, Application US/09252991A

; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 27366  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27366

Query Match 90.0%; Score 27; DB 4; Length 231;  
Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
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Db 203 EELQRR 208

RESULT 13  
US-09-902-540-13879  
; Sequence 13879, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 13879  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-13879

Query Match 90.0%; Score 27; DB 4; Length 291;  
Best Local Similarity 83.3%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||  
Db 249 EELQRR 254

RESULT 14  
US-09-543-681A-5695  
; Sequence 5695, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 5695  
; LENGTH: 314  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-5695

Query Match 90.0%; Score 27; DB 4; Length 314;  
Best Local Similarity 83.3%; Pred. No. 5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6  
Db 135 EELQRR 140

## RESULT 15

US-07-803-622E-7  
; Sequence 7, Application US/07803622E  
; Patent No. 5525497  
; GENERAL INFORMATION:  
; APPLICANT: Keller, Walter  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Martin, Georges  
; APPLICANT: Wahle, Elmar  
; TITLE OF INVENTION: RECOMBINANT POLY(A) POLYMERASE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/803,622E  
; FILING DATE: 27-NOV-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 195/296  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 213-489-1600  
; TELEFAX: 213-955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 375 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-803-622E-7

Query Match 90.0%; Score 27; DB 1; Length 375;  
Best Local Similarity 83.3%; Pred. No. 5.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6  
Db 56 EELQRR 61

Search completed: February 5, 2005, 23:24:47  
Job time : 44 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2005, 23:12:52 ; Search time 129 Seconds  
(without alignments)  
15.149 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA.\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US04\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US03\_PUBCOMB.pep.\*
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- 7: /cgn2\_6/ptodata/2/pubpaa/US01\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US00\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/ptodata/2/pubpaa/US04\_PUBCOMB.pep.\*
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- 16: /cgn2\_6/ptodata/2/pubpaa/US02\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US00\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	30	100.0	93	US-10-282-122A-71377	Sequence 71377, A
2	30	100.0	206	US-09-942-024-2	Sequence 2, Appli
3	30	100.0	206	US-09-942-024-7	Sequence 7, Appli
4	30	100.0	206	US-09-942-024-12	Sequence 12, Appl
5	30	100.0	206	US-09-942-024-2	Sequence 2, Appli
6	30	100.0	206	US-09-942-024-7	Sequence 7, Appli
7	30	100.0	206	US-09-942-024-12	Sequence 12, Appl
8	30	100.0	206	US-10-261-161-4	Sequence 4, Appli
9	30	100.0	206	US-10-261-161-5	Sequence 5, Appli
10	30	100.0	206	US-10-261-161-109	Sequence 109, App
11	30	100.0	206	US-10-318-417-3	Sequence 3, Appli
12	30	100.0	249	US-09-942-024-16	Sequence 16, Appl
13	30	100.0	249	US-09-942-024-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-10-282-122A-71377

Sequence 71377, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Cart, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

Sequence 9, Appli  
Sequence 21, Appli  
Sequence 255, App  
Sequence 162440,  
Sequence 179345,  
Sequence 208350,  
Sequence 186497,  
Sequence 144759,  
Sequence 237624,  
Sequence 141286,  
Sequence 43626, A  
Sequence 1287, Ap  
Sequence 106246,  
Sequence 131892,  
Sequence 33812, A  
Sequence 791, App  
Sequence 791, App  
Sequence 74647, A  
Sequence 66793, A  
Sequence 60379, A  
Sequence 40902, A  
Sequence 246623,  
Sequence 141287,  
Sequence 165851,  
Sequence 67873, A  
Sequence 192256,  
Sequence 103645,  
Sequence 10629, A  
Sequence 154851,  
Sequence 4653, Ap  
Sequence 237591,

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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71377
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71377

Query Match      100.0%; Score 30; DB 15; Length 93;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
        |||||
Db      24 EEMQRR 29

RESULT 2
US-09-942-024-2
; Sequence 2, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-2

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
        |||||
Db      12 EEMQRR 17

RESULT 3
US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
        |||||
Db      12 EEMQRR 17

RESULT 4
US-09-942-024-12
; Sequence 12, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-12

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
        |||||
Db      12 EEMQRR 17

RESULT 5
US-09-942-098-2
; Sequence 2, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-2

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
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Db      12 EEMQRR 17

RESULT 6
US-09-942-098-7
; Sequence 7, Application US/09942098
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; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: FRET Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-098-7

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

RESULT 7
US-09-942-098-12
; Sequence 12, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: FRET Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-12

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

US-09-942-098-12
; Sequence 12, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: FRET Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-12

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

US-10-261-161-4
; Sequence 4, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-261-161-4

Query Match      100.0%; Score 30; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

US-10-261-161-5
; Sequence 5, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-261-161-5

Query Match      100.0%; Score 30; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

US-10-261-161-109
; Sequence 109, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-261-161-109

Query Match      100.0%; Score 30; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17
```

```
RESULT 11
US-10-318-417-3
; Sequence 3, Application US/10318417
; Publication No. US20040115727A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Evolved Clostridial Toxins With Altered
; TITLE OF INVENTION: Protease Specificity
; FILE REFERENCE: P-AR 4670
; CURRENT APPLICATION NUMBER: US/10/318,417
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-417-3
Query Match 100.0%; Score 30; DB 16; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
Db 12 EEMQRR 17
|||||

RESULT 12
US-09-942-024-16
; Sequence 16, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-024-16
Query Match 100.0%; Score 30; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
Db 12 EEMQRR 17
|||||

RESULT 13
US-09-942-098-16
; Sequence 16, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-098-16
Query Match 100.0%; Score 30; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
Db 12 EEMQRR 17
|||||

RESULT 14
US-10-261-161-9
; Sequence 9, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-261-161-9
Query Match 100.0%; Score 30; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
Db 12 EEMQRR 17
|||||

RESULT 15
US-10-029-217A-21
; Sequence 21, Application US/10029217A
; Publication No. US20020164735A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC N.
; APPLICANT: WANG, DA-ZHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
; TITLE OF INVENTION: NUCLEAR REGULATORY FACTOR
; FILE REFERENCE: UTSD:695US
; CURRENT APPLICATION NUMBER: US/10/029,217A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/257,761
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-217A-21
Query Match 90.0%; Score 27; DB 13; Length 35;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 EEMQRR 6  
| | | |  
Db 11 EELQRR 16

Search completed: February 5, 2005, 23:27:28  
Job time : 130 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 5, 2005, 22:37:00 ; Search time 38 seconds  
(without alignments)  
15.192 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	56	2 S36812	probable synapse-a
2	30	100.0	149	2 D95399	protein [imported]
3	30	100.0	206	2 A37861	synaptosomal-assoc
4	30	100.0	206	2 I53735	nerve terminal pro
5	30	100.0	206	2 I67823	synaptosomal-assoc
6	30	100.0	206	2 A33623	SNAP-25 protein -
7	30	100.0	249	2 S38308	SNAP-25 protein -
8	30	100.0	249	2 S38309	SNAP-25 protein -
9	27	90.0	112	2 T34589	hypothetical prote
10	27	90.0	117	2 C87594	hypothetical prote
11	27	90.0	162	1 F70358	hydrogenase matura
12	27	90.0	257	2 C83005	conserved hypothet
13	27	90.0	264	2 D75298	carbonic anhydrase
14	27	90.0	283	2 S42393	G-box-binding prot
15	27	90.0	303	2 S58243	Pyroloquinoline q
16	27	90.0	309	2 E69200	conserved hypothet
17	27	90.0	319	2 C83892	proline dehydrogen
18	27	90.0	337	2 T06602	hypothetical prote
19	27	90.0	333	2 T05121	hypothetical prote
20	27	90.0	378	2 JC5658	LiM domain-contain
21	27	90.0	407	2 C97212	HD GYP hydrolase d
22	27	90.0	450	2 C75033	adenylosuccinate l
23	27	90.0	450	2 H71135	probable adenylosu
24	27	90.0	453	2 S52690	hypothetical prote
25	27	90.0	472	2 AB3239	conserved hypothet
26	27	90.0	509	2 A71254	probable glu-tRNA
27	27	90.0	528	2 B75310	conserved hypothet
28	27	90.0	534	2 T39903	serine-rich protei
29	27	90.0	622	2 S51972	SPC72 protein - ye

30 27 90.0 647 2 C71534 probable transglyc  
31 27 90.0 689 2 S17875 polynucleotide ade  
32 27 90.0 702 2 C69999 DNA translocase et  
33 27 90.0 727 2 S54512 hypothetical prote  
34 27 90.0 739 2 S18642 polynucleotide ade  
35 27 90.0 740 2 S17925 polynucleotide ade  
36 27 90.0 783 2 AF1275 DNA translocase ho  
37 27 90.0 784 2 AF1638 DNA translocase ho  
38 27 90.0 809 1 Q0BE34 BBLF4 protein - hu  
39 27 90.0 856 2 T13159 E1B-sskba-associa  
40 27 90.0 869 2 A25945 coagulation factor  
41 27 90.0 947 2 B86231 hypothetical prote  
42 27 90.0 961 2 A55380 facio-genital dyspl  
43 27 90.0 1203 2 T21275 hypothetical prote  
44 27 90.0 1274 2 A89959 hypothetical prote  
45 27 90.0 1328 2 AE2351 protoporphyrin IX

## ALIGNMENTS

### RESULT 1

S36812

probable synapse-associated 28K protein - bovine (fragments)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 07-May-1999

C;Accession: S36812

R;Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T

FEBS Lett. 330, 236-240, 1993

A;Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presy

A;Reference number: S36811; MUID:93374072; PMID:8365494

A;Accession: S36812

A;Molecule type: protein

A;Residues: 1-56 <HOR>

A;Experimental source: brain

Query Match 100.0%; Score 30; DB 2; Length 56;

Best Local Similarity 100.0%; Pred. No. 8.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6

DB 2 EEMQRR 7

### RESULT 2

D95399

protein [imported] - Sinorhizobium meliloti (strain 1021) magaplaamid pSymA

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C;Accession: D95399

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9886, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: D95399

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-149 <KUR>

A;Cross-references: UNIPROT:Q92XY8; GB:AE006469; PIDN:AAK65758.1; PID:g14524256; GSPDB:

A;Experimental source: strain 1021, megaplaamid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler

peira, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure

hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: SMA2009

A;Genome: plasmid

Query Match 100.0%; Score 30; DB 2; Length 149;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||||

Db 137 EEMQRR 142

#### RESULT 3

A37861  
synaptosomal-associated 25K protein - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 09-Jul-2004  
C;Accession: A37861  
R;Catsicag, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991  
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides with the expression of synaptophysin in the developing rat brain.  
A;Reference number: A37861; MUID:91126080; PMID:1992470  
A;Accession: A37861  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-206 <CAT>  
A;Cross-references: UNIPROT:P60878; GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match 100.0%; Score 30; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||||

Db 12 EEMQRR 17

#### RESULT 4

I53735  
nerve terminal protein - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I53735  
R;Bark, I.C.; Wilson, M.C.  
Gene 139, 291-292, 1994  
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein.  
A;Reference number: I53735; MUID:94156217; PMID:8112622  
A;Accession: I53735  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-206 <RES>  
A;Cross-references: UNIPROT:P60880; GB:L19760; NID:g307425; PIDN:AAC37545.1; PID:g307426  
C;Genetics:  
A;Gene: GDB:SNAP  
A;Cross-references: GDB:355671; OMIM:600322  
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 30; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||||

Db 12 EEMQRR 17

#### RESULT 5

I67823  
nerve terminal protein - human  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I67823  
R;Bark, I.C.; Wilson, M.C.  
Gene 139, 291-292, 1994.

A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein.  
A;Reference number: I53735; MUID:94156217; PMID:8112622  
A;Accession: I67823  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-206 <RES>  
A;Cross-references: UNIPROT:P60880; GB:L19761; NID:g307427; PIDN:AAC37546.1; PID:g307428  
C;Genetics:  
A;Gene: GDB:SNAP  
A;Cross-references: GDB:355671; OMIM:600322  
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 30; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||||

Db 12 EEMQRR 17

#### RESULT 6

A33623  
synaptosomal-associated 25K protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 04-Apr-1990 #sequence\_revision 04-Apr-1990 #text\_change 09-Jul-2004  
C;Accession: A33623  
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; J. Cell Biol. 109, 3039-3052, 1989  
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differs from synaptophysin.  
A;Reference number: A33623; MUID:90078337; PMID:2592413  
A;Accession: A33623  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-206 <OYL>  
A;Cross-references: UNIPROT:P60879; GB:M22012; GB:X51673; NID:g200997; PIDN:AAA61741.1;

Query Match 100.0%; Score 30; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||||

Db 12 EEMQRR 17

#### RESULT 7

S38308  
SNAP-25 protein - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 09-Jun-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
C;Accession: S38308  
R;Bark, I.C.  
J. Mol. Biol. 233, 67-76, 1993  
A;Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding di- and tripeptide repeats.  
A;Reference number: S38308; MUID:93389738; PMID:8377193  
A;Accession: S38308  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-249 <BAR>  
A;Cross-references: EMBL:L09250  
C;Genetics:  
A;Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 30; DB 2; Length 249;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||||

Db 12 EEMQRR 17



## RESULT 8

S38309  
SNAP-25 protein - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 09-Jun-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
C;Accession: S38309  
R;Bark, I.C.  
J. Mol. Biol. 233, 67-76, 1993  
A;Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding disulfide isomerase  
A;Reference number: S38308; MUID:93389738; PMID:8377193  
A;Accession: S38309  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-249 <BAR>  
A;Cross-references: EMBL:L09250  
C;Genetics:  
A;Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 30; DB 2; Length 249;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||  
Db 12 EEMQRR 17

## RESULT 9

T34589  
hypothetical protein SC10A5.22 SC10A5.22 - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C;Accession: T34589  
R;Murphy, L.; Harris, D.; Parthill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1998  
A;Reference number: Z21548  
A;Accession: T34589  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-112 <MUR>  
A;Cross-references: UNIPROT:O54113; EMBL:AL021529; PIDN:CAA16454.1; GSPDB:GN000070; SCORE  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SCOEDB:SC10A5.22

Query Match 90.0%; Score 27; DB 2; Length 112;  
Best Local Similarity 83.3%; Pred. No. 73;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||  
Db 97 EELQRR 102

## RESULT 10

C87594  
hypothetical protein CC3787 [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C;Accession: C87594  
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of Caulobacter crescentus.  
A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: C87594  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-117 <STO>  
A;Cross-references: UNIPROT:Q9MAP3; GB:AE005673; MID:gl3424387; PIDN:AAK24751.1; GSPDB:G  
C;Genetics:  
A;Gene: CC2787

Query Match 90.0%; Score 27; DB 2; Length 117;  
Best Local Similarity 83.3%; Pred. No. 76;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||  
Db 74 DEMQRR 79

## RESULT 11

F70358  
hydrogenase maturation factor hupD [similarity] - Aquifex aeolicus  
C;Species: Aquifex aeolicus  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 17-Mar-2003  
C;Accession: F70358  
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; S  
V.

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A;Reference number: A70300; MUID:98196666; PMID:9537320  
A;Accession: F70358

A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-162 <AQF>

A;Cross-references: GB:AE000701; GB:AE000657; MID:g2983260; PIDN:AAC06858.1; PID:g29832

A;Experimental source: strain VF5

C;Genetics:

A;Gene: hupD

C;Superfamily: [NiFe]-hydrogenase maturation protease

Query Match 90.0%; Score 27; DB 1; Length 162;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||  
Db 23 EELQRR 28

## RESULT 12

C83005  
conserved hypothetical protein PA5135 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: C83005  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: C83005  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-257 <STO>  
A;Cross-references: UNIPROT:Q9HU49; GB:AE004926; GB:AE004091; MID:g9951424; PIDN:AAG085  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA5135

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: C83005

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-257 <STO>

A;Cross-references: UNIPROT:Q9HU49; GB:AE004926; GB:AE004091; MID:g9951424; PIDN:AAG085

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA5135

Query Match 90.0%; Score 27; DB 2; Length 257;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
|||  
Db 143 EELQRR 148

## RESULT 13

D75298  
carbonic anhydrase - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: D75298  
R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 266, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: D75298  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-264 <WHI>  
A;Cross-references: UNIPROT:Q9RS89; GB:AE002056; GB:AE000513; NID:g6460037; PIDN:AAF1178  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR2238  
A;Map position: 1  
C;Superfamily: Escherichia coli carbonate dehydratase

Query Match 90.0%; Score 27; DB 2; Length 264;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
||:||||  
DB 34 EELQRR 39

## RESULT 14

S42393  
G-box-binding protein - tomato  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S42393  
R;Meier, I.; Gruissem, W.  
Nucleic Acids Res. 22, 470-478, 1994  
A;Title: Novel conserved sequence motifs in plant G-box binding proteins and implication  
A;Reference number: S42392; MUID:94173701; PMID:8127687  
A;Accession: S42393  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-283 <MEI>  
A;Cross-references: UNIPROT:Q43508; EMBL:X74942; NID:g456752; PIDN:CAA52896.1; PID:g4567  
C;Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology  
F;182-222/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match 90.0%; Score 27; DB 2; Length 283;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
||:||||  
DB 213 EELQRR 218

## RESULT 15

S58243  
pyrroloquinoline quinone synthesis B - Pseudomonas fluorescens  
C;Species: Pseudomonas fluorescens  
C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C;Accession: S58243  
R;Schneider, U.; Keel, C.; Defago, G.; Haas, D.  
submitted to the EMBL Data Library, May 1995  
A;Description: Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0: the  
A;Reference number: S58239  
A;Cross-references: UNIPROT:P55172; EMBL:X87299; NID:g929799; PIDN:CAA60733.1; PID:g9298  
A;Residues: 1-303 <SCH>

Query Match 90.0%; Score 27; DB 2; Length 303;

Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
||:||||  
DB 227 DEMQRR 232

Search completed: February 5, 2005, 23:12:47  
Job time : 39 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 5, 2005, 23:02:51 ; Search time 170 Seconds  
(without alignments)

18.073 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	18	2 Q9TRF1	Q9trf1 bos taurus
2	30	100.0	82	2 Q8IQC6	Q8iqc6 drosophila
3	30	100.0	82	2 Q8MZ33	Q8mz33 drosophila
4	30	100.0	107	2 Q8N3E7	Q8n3e7 homo sapien
5	30	100.0	149	2 Q92XY8	Q92xy8 rhizobium m
6	30	100.0	166	2 Q6QNZ0	Q6qnz0 poephila gu
7	30	100.0	206	1 SN25 CHICK	P60878 gallus gall
8	30	100.0	206	1 SN25 HUMAN	P60880 homo sapien
9	30	100.0	206	1 SN25 MACMU	P60877 macaca mula
10	30	100.0	206	1 SN25 MOUSE	P60879 mus musculus
11	30	100.0	206	1 SN25 RAT	P60881 rattus norv
12	30	100.0	206	2 Q8AXM1	Q8axm1 xenopus lae
13	30	100.0	206	2 Q8AXM2	Q8axm2 xenopus lae
14	30	100.0	206	2 Q640W4	Q640w4 xenopus lae
15	30	100.0	216	2 Q7Z390	Q7z390 homo sapien
16	30	100.0	284	2 Q67XD8	Q67kd8 symbiobacte
17	30	100.0	297	2 Q8N417	Q8n417 homo sapien
18	30	100.0	344	2 Q6BYE0	Q6bye0 debaryomyce
19	30	100.0	507	2 Q86VG8	Q86vg8 homo sapien
20	30	100.0	537	2 Q9W2P0	Q9w2p0 drosophila
21	30	100.0	571	2 Q68D10	Q68d10 homo sapien
22	30	100.0	576	2 Q6AS79	Q6as79 desulfotale
23	30	100.0	616	2 Q6AWAS	Q6awas homo sapien
24	30	100.0	685	2 Q6MZ15	Q6mz15 homo sapien
25	30	100.0	739	2 Q7XR86	Q7xtr86 oryza sativ
26	30	100.0	753	2 Q6BGL9	Q6bgl9 paramecium
27	30	100.0	904	2 Q8IWC1	Q8iwc1 homo sapien
28	30	100.0	1142	2 Q757D1	Q757d1 ashbya goss
29	27	90.0	21	2 Q875B3	Q875b3 chimpanzee
30	27	90.0	81	2 Q7V6N4	Q7v6n4 prochlorococ
31	27	90.0	87	2 Q69YU4	Q69yu4 homo sapien

## RESULT 1

Q9TRF1 ID Q9TRF1 PRELIMINARY; PRT; 18 AA.  
AC Q9TRF1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Soluble N-ethylmaleimide-sensitive attachment protein SNAP-25  
(Fragment).  
DE (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93374072; PubMed=8365494; DOI=10.1016/0014-5793(93)80281-X;  
RA Horikawa H.P., Saisu H., Ishizuka T., Sekine Y., Tugita A., Odani S.,  
RA Abe T.;  
RL FEBS Lett. 330:236-240(1993).  
SQ SEQUENCE 18 AA; 2120 MW; 371FC93766CA7BB CRC64;

Query Match 100.0%; Score 30; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6

Db 2 EEMQRR 7

## RESULT 2

Q8IQC6 ID Q8IQC6 PRELIMINARY; PRT; 82 AA.  
AC Q8IQC6;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE CG32039-PA.  
GN ORFNames=CG32039;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlie C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laško P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Smith T.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith H.,  
 RA Spier R., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*";  
 RL Science 287:2185-2195(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoekins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
 RT *melanogaster* euchromatic genome sequence";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomics perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Mirza S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review";  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003552; J011959.1; --  
 DR FlyBase; FBgn0052039; CG32039.  
 SQ SEQUENCE 82 AA; 9540 MW; E0FE73104AC0796E CRC64;  
 Query Match 100.0%; Score 30; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EEMQRR 6  
 Db 58 EEMQRR 63  
 RESULT 3  
 Q8MZ33 PRELIMINARY; PRT; 82 AA.  
 AC Q8MZ33;  
 DT 01-OCT-2002 (TREMELrel. 22, Created)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DT 01-OCT-2004 (TREMELrel. 26, Last annotation update)  
 DE RE03722p.  
 GN ORFNames=CG32039;  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champagne M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY113381; J013386.1; --  
 DR FlyBase; FBgn0052039; CG32039.  
 SQ SEQUENCE 82 AA; 9539 MW; E0F4D3104060796E CRC64;  
 Query Match 100.0%; Score 30; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EEMQRR 6  
 Db 58 EEMQRR 63  
 RESULT 4  
 Q8N3E7 PRELIMINARY; PRT; 107 AA.  
 AC Q8N3E7;  
 DT 01-OCT-2002 (TREMELrel. 22, Created)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DE Hypothetical protein DKFZp76111323 (Fragment).  
 GN Name=DKFZp76111323;  
 OS *Homo sapiens* (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Amalgam;  
 RG The German cDNA Consortium;  
 RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,  
 RA Osanger A., Fobo G., Han M., Wiemann S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL834393; J0139055.1; --  
 KW Hypothetical protein.

```
FT NON TER 1 1
SQ SEQUENCE 107 AA; 13460 MW; A411B3F036789795 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 94 EEMQRR 99

RESULT 5
Q92XY8 PRELIMINARY; PRT; 149 AA.
AC Q92XY8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN ORFNames=SMa2009;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barlow-Hubler F., Bowler L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Rederpsiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
RM EMBL; AE007296; AAK65758.1; -.
DR PIR; D95399; D95399.
DR InterPro; IPR004360; Gly_bleo_diox.
DR Pfam; PF00903; Glyoxalase; 1.
SQ SEQUENCE 149 AA; 16237 MW; 86C045BFD8F5ACF5 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 137 EEMQRR 142

RESULT 6
Q6QN20 PRELIMINARY; PRT; 166 AA.
AC Q6QN20;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SNAP-25b (Fragment).
OS Poephila guttata (Zebra finch) (Taeniopygia guttata).
OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Estrildinae; Taeniopygia.
OX NCBI_TaxID=59729;
RN [1]
RP SEQUENCE FROM N.A.
RA Voigt C., Metzendorf R., Gahr M.;
RT "Differential expression pattern and steroid hormone sensitivity of
RT SNAP-25 and synapoporin mRNA in the telencephalic song control
RT nucleus HVC of the zebra finch.";
```

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RL J. Comp. Neurol. 0:0-0 (2004).
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
DR EMBL; AV531112; AAS21684.1; -.
DR GO; GO:0019717; C-synaptoosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR010989; t-snare.
DR InterPro; IPR000727; t-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 1.
DR PROSITE; PS50192; t-SNARE; 2.
KW Synaptoosome.
FT NON_TER 1 1
FT NON_TER 166 166
SQ SEQUENCE 166 AA; 18793 MW; 04F06E677D7BC1C7 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 5 EEMQRR 10

RESULT 7
SN25 CHICK STANDARD; PRT; 206 AA.
ID SN25 CHICK
AC P60878; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Synaptoosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SNAP25B).
RC STRAIN=White leghorn; TISSUE=Retina;
RX MEDLINE=91126080; PubMed=192470;
RX Catsicas S., Larhammer D., Blomqvist A.G., Sanna P.P., Milner R.J.,
RX Wilson M.C.;
RA "Expression of a conserved cell-type-specific protein in nerve
RA terminals coincides with synaptogenesis."
RT Proc. Natl. Acad. Sci. U.S.A. 88:785-789 (1991).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORMS SNAP25A AND SNAP25B).
RX MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RT encoding distinct isoforms of the protein."
RL J. Mol. Biol. 233:67-76 (1993).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXB6 (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60878-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60878-2, P13795-2;
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CC      Sequence=VSP 010018;
CC      -|- PTM: Palmitoylated (By similarity).
CC      -|- SIMILARITY: Belongs to the SNAP-25 family.
CC      -|- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR EMBL; M57957; AAA49072.1; -.
DR EMBL; L09253; AAA49070.1; -.
DR EMBL; L09254; AAA49070.1; JOINED.
DR EMBL; L09257; AAA49070.1; JOINED.
DR EMBL; L09259; AAA49070.1; JOINED.
DR EMBL; L09251; AAA49070.1; JOINED.
DR EMBL; L09258; AAA49070.1; JOINED.
DR EMBL; L09250; AAA49070.1; JOINED.
DR EMBL; L09253; AAA49071.1; -.
DR EMBL; L09254; AAA49071.1; JOINED.
DR EMBL; L09257; AAA49071.1; JOINED.
DR EMBL; L09259; AAA49071.1; JOINED.
DR EMBL; L09252; AAA49071.1; JOINED.
DR EMBL; L09256; AAA49071.1; JOINED.
DR EMBL; L09250; AAA49071.1; JOINED.
DR PIR; A37861; A37861.
DR GO; GO:0007269; P:neurotransmitter secretion; NAS.
DR GO; GO:0001504; P:neurotransmitter uptake; NAS.
DR GO; GO:0007268; P:synaptic transmission; NAS.
DR GO; GO:0016081; P:synaptic vesicle docking; NAS.
DR InterPro; IPR000928; t-SNAP-25.
DR PROSITE; PS50192; t-SNARE; 2.
KW Alternative splicing; Coiled coil; Lipoprotein; Palmitate; Repeat;
KW Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1;
FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
FT SITE 85 92 Cys-rich.
FT SITE 180 181 Cleavage (by BONT/E) (By similarity).
FT VARSPLIC 58 89 ETEEGMDQINKDMKEAKNLTDLGKFGCLGV -> DRVVEE
FT FT GNHINQDMKEAKNLDKLGKCGFLI (in isoform
FT FT SNAP-25a).
FT FT /FTID=VSP_010018.
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 30; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
Db 12 EEMQRR 17
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RESULT 8
SN25 HUMAN STANDARD; PRT; 206 AA.
ID P08080; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
AC P08080; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
RC TISSUE=Brain;
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RX MEDLINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0;
RA Bark I.C., Wilson M.C.;
RT "Human cDNA clones encoding two different isoforms of the nerve
RL terminal protein SNAP-25.";
RL Gene 139:291-292 (1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).
RC TISSUE=Brain;
RX MEDLINE=94333829; PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2;
RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;
RT "Cloning and sequence analysis of the human SNAP25 cDNA.";
RL Gene 145:313-314 (1994).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Skeletal muscle;
RX MEDLINE=96332494; PubMed=8760387;
RA Jagadeesh M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
RA Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
RA Ward C.W.;
RT "Insulin-responsive tissues contain the core complex protein SNAP-25
(synaptosomal-associated protein 25) A and B isoforms in addition to
syntaxin 4 and synaptobrevins 1 and 2.";
RL Biochem. J. 317:945-954 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Gramham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huxley E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kacy M.P., Kimberley A.M., King A., Knights A., Laird G.M., Lawlor S.,
RA Leivaesalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.D., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilting L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871 (2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Maman A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smolius D.E.,
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6  
DB 12 EEMQRR 17

RESULT 10  
SN25 MOUSE  
ID SN25 MOUSE STANDARD; PRT; 206 AA.  
AC P60879; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Synaptoosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).  
GN Name-Snap25; Synonyms=Snap;  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC STRAIN=BALB/c;  
RX MEDLINE=90078337; PubMed=2522413; DOI=10.1083/jcb.109.6.3039;  
RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,  
Bloom F.E., Wilson M.C.;  
RT "The identification of a novel synaptoosomal-associated protein, SNAP-  
25, differentially expressed by neuronal subpopulations.";  
RL J. Cell Biol. 109:3039-3052(1989).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC STRAIN=ILS, and ISS;  
RX MEDLINE=21363810; PubMed=11471062;  
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,  
Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;  
RT "High-throughput sequence identification of gene coding variants  
within alcohol-related QTLs.";  
RL Mamm. Genome 12:657-663(2001).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).  
RC STRAIN=C57BL/6J; Tissue=Medulla oblongata;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
Gaasterland T., Gariboldi M., Glissi C., Godzik A., Gough J.,  
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
Kana A., Kawai H., Kawasawa Y., Kedziarski R.M., King B.L.,  
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,  
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,  
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).

RC STRAIN=C57BL/6; Tissue=Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP INTERACTION WITH SNAP25BP.  
RX PubMed=10195194; DOI=10.1038/5673;  
RA Ilardi J.M., Mochida S., Sheng Z.H.;  
RT "Snapin: a SNARE-associated protein implicated in synaptic  
transmission.";  
RL Nat. Neurosci. 2:119-124(1999).  
CC -!- FUNCTION: t-SNARE involved in the molecular regulation of  
neurotransmitter release. May play an important role in the  
synaptic function of specific neuronal systems. Associates with  
proteins involved in vesicle docking and membrane fusion.  
CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2  
and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1  
and SNAP25BP. Binds STXBP6 (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Comment=isoforms differ by the usage of two alternative  
homologous exons (5a and 5b) which encode for positions 56 to 94  
and differ only in 9 positions out of 39;  
CC Name=SNAP-25b;  
CC IsoId=P60879-1, P13795-1;  
CC Sequence=Displayed;  
CC Name=SNAP-25a;  
CC IsoId=P60879-2, P13795-2;  
CC Sequence=VSP 010019;  
CC -!- PTM: palmitoylated (By similarity).  
CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL; M22012; AAA61741.1; -;  
CC EMBL; AF483516; AAL90790.1; -;  
CC EMBL; AF483517; AAL90791.1; -;  
CC EMBL; AK078038; AAC37105.1; -;  
CC EMBL; BC018249; AAL18249.1; -;  
CC PIR; A33623; A33623.  
CC MGD; MGI:98331; Snap25.  
CC GO; GO:0007269; P:neurotransmitter secretion; NAS.  
CC GO; GO:0001504; P:neurotransmitter uptake; NAS.  
CC GO; GO:0007268; P:synaptic transmission; NAS.  
CC GO; GO:0016081; P:synaptic vesicle docking; NAS.  
CC InterPro; IPR000928; SNAP-25.  
CC InterPro; IPR000727; T\_SNARE.  
CC PROSITE; PS50192; T\_SNARE; 2.



KW Alternative splicing; Coiled coil; Lipoprotein; Palmitate; Repeat;  
 KW Synaptosome.  
 FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.  
 FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.  
 FT DOMAIN 85 92 Cys-rich.  
 FT SITE 180 181 Cleavage (by BONT/E) (By similarity).  
 FT VARSPLIC 58 89 ERIBEGMDQINKMKAEKNLDIGKFCGLCV -> DRVBE  
 FT FT GMNHINQDMKEAKENLDIGKFCGLFI (in isoform  
 FT SNAP-25a).  
 FT FT /FTid=VSP\_010019.  
 SQ SEQUENCE 206 AA; 23315 MW; PBD2B082A4CB6A6 CRC64;  
 Query Match 100.0%; Score 30; DB 1; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EEMQRR 6  
 DB 12 EEMQRR 17  
 RESULT 11  
 SN25\_RAT  
 ID SN25\_RAT STANDARD; PRT; 206 AA.  
 AC P60881; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).  
 GN Name=Snap25; Synonyms=Snap;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).  
 RA Kataoka M.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
 RC TISSUE=Brain;  
 RA Cho A.R., You K.H.;  
 RL "Cloning of the SNAP-25 gene from a rat brain cDNA library."  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).  
 RC TISSUE=Brain;  
 RX MEDLINE=99155074; PubMed=10037470;  
 RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.B.;  
 RT "SNARE complex proteins, including the cognate pair VAMP-2 and  
 RT syntaxin-4, are expressed in cultured oligodendrocytes."  
 RL J. Neurochem. 72:988-998(1999).  
 RN [4]  
 RP PALMITOYLATION.  
 RX MEDLINE=93100552; PubMed=1281490;  
 RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;  
 RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major  
 RT methionine-rich polypeptide in rapid axonal transport and a major  
 RT substrate for palmitoylation in adult CNS."  
 RL J. Neurosci. 12:4634-4641(1992).  
 RN [5]  
 RP SUBCELLULAR LOCATION OF RNA TRANSCRIPTS.  
 RX MEDLINE=96346613; PubMed=8738135; DOI=10.1016/0169-328X(95)00272-T;  
 RA Jacobsson G., Pielh F., Bark I.C., Zhang X., Meister B.;  
 RT "Differential subcellular localization of SNAP-25a and SNAP-25b RNA  
 RT transcripts in spinal motoneurons and plasticity in expression after  
 RT nerve injury."  
 RL Brain Res. Mol. Brain Res. 37:49-62(1996).  
 RN [6]  
 RP INTERACTION WITH RIMS1.  
 RX MEDLINE=21413925; PubMed=11438518; DOI=10.1074/jbc.M100929200;  
 RA Coppola T., Magnin-Luethi S., Perret-Menoud V., Gattesco S.,  
 RA Schiavo G., Regazzi R.

RT "Direct interaction of the Rab3 effector RIM with Ca2+ channels, SNAP-  
 RT 25, and synaptotagmin."  
 RL J. Biol. Chem. 276:32756-32762(2001).  
 RN [7]  
 RP INTERACTION WITH STXBp6.  
 RX MEDLINE=22140381; PubMed=12145319; DOI=10.1074/jbc.M204929200;  
 RA Scales S.J., Heiser B.A., Masuda E.S., Scheller R.H.;  
 RT "Amisyn, a novel syntaxin-binding protein that may regulate SNARE  
 RT complex assembly."  
 RL J. Biol. Chem. 277:28271-28279(2002).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-83 AND 120-206 IN COMPLEX  
 RP WITH STX1A AND VAMP2.  
 RX MEDLINE=98430524; PubMed=9759724; DOI=10.1038/26412;  
 RA Sutton R.B., Faehauer D., Jahn R., Brunger A.T.;  
 RT "Crystal structure of a SNARE complex involved in synaptic exocytosis  
 RT at 2.4 A resolution."  
 RL Nature 395:347-353(1998).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-83 IN COMPLEX WITH STX1A.  
 RX MEDLINE=21538870; PubMed=11533035; DOI=10.1074/jbc.M106853200;  
 RA Misura K.M.S., Gonzalez L.C. Jr., May A.P., Scheller R.H., Weiss W.I.;  
 RT "Crystal structure and biophysical properties of a complex between the  
 RT N-terminal SNARE region of SNAP25 and syntaxin 1a."  
 RL J. Biol. Chem. 276:41301-41309(2001).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 7-83 AND 141-204 IN COMPLEX  
 RP WITH STX1A AND VAMP2.  
 RX MEDLINE=22499607; PubMed=12496247; DOI=10.1074/jbc.M211889200;  
 RA Ernst J.A., Brunger A.T.;  
 RT "High resolution structure, stability, and synaptotagmin binding of a  
 RT truncated neuronal SNARE complex."  
 RL J. Biol. Chem. 278:8630-8636(2003).  
 CC -I- FUNCTION: t-SNARE involved in the molecular regulation of  
 CC neurotransmitter release. May play an important role in the  
 CC synaptic function of specific neuronal systems. Associates with  
 CC proteins involved in vesicle docking and membrane fusion.  
 CC -I- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2  
 CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1  
 CC and SNAP25BP. Binds STXBp6.  
 CC -I- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Isoforms differ by the usage of two alternative  
 CC homologous exons (5a and 5b) which encode for positions 56 to 94  
 CC and differ only in 9 positions out of 39;  
 CC Name=SNAP-25b;  
 CC IsoId=P60881-1, P13795-1;  
 CC Sequences=2a;  
 CC Name=SNAP-25a;  
 CC IsoId=P60881-2, P13795-2;  
 CC Sequences=VSP\_010020;  
 CC -I- PTM: Palmitoylated.  
 CC -I- SIMILARITY: Belongs to the SNAP-25 family.  
 CC -I- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
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 CC -----  
 CC EMBL; AB003991; BAA20151.1; -;  
 CC EMBL; AB003992; BAA20152.1; -;  
 CC EMBL; AF245227; AAF81202.1; -;  
 CC EMBL; U56262; AAA99826.1; -;  
 CC EMBL; U56261; AAA99825.1; -;  
 CC PDB; 1JTH; X-ray; -;  
 CC PDB; 1N7S; X-ray; -;  
 CC PDB; 1SFC; X-ray; -;  
 CC PDB; 2BU0; Model; -;  
 CC RGD; 3728; Snap25.

DR GO: GO:0007269; P:neurotransmitter secretion; NAS.  
DR GO: GO:0001504; P:neurotransmitter uptake; NAS.  
DR GO: GO:0007268; P:synaptic transmission; NAS.  
DR GO: GO:0016081; P:synaptic vesicle docking; NAS.  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T SNARE.  
DR PROSITE: PS0192; T SNARE; 2.  
KW 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;  
KW Palmitate; Repeat; Synaptosome.  
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.  
FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.  
FT DOMAIN 85 92 Cys-rich.  
FT SITE 180 181 Cleavage (by BONT/E) (by similarity).  
FT VARSPIC 58 89 ERLEGGDQINKMEKXNLDLGEQGLCV -> DRVVEE  
FT GNNHINQDMKEAKNLDLKGCCGLFI (in isoform  
FT /FTID=VSP\_010020.  
FT HELIX 7 82  
FT HELIX 142 201  
FT TURN 202 202  
FT TURN 202 202  
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;  
Query Match 100.0%; Score 30; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EEMQRR 6  
DB 12 EEMQRR 17  
RESULT 12  
Q8AXM1 PRELIMINARY; PRT; 206 AA.  
AC Q8AXM1;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE SNAP25b (Snap25-prov protein).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshikiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]

RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";  
RN Dev. Dyn. 225:384-391 (2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX Klein S., Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
DR EMBL; AF335587; AA033789.1; -.  
DR EMBL; BC055981; AAHS5981.1; -.  
DR HSSP; P60881; 1JTH.  
DR GO: GO:0019717; C:synaptosome; IEA.  
DR GO: GO:0003700; P:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR002197; HTH\_Fis.  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR010989; t-snare.  
DR InterPro: IPR000727; T SNARE.  
DR Pfam; PF00835; SNAP-25; 1.  
DR Pfam; PF05739; SNARE; 1.  
DR PRINTS; PRO1590; HTHFIS.  
DR SMART; SM00397; t-SNARE; 2.  
DR PROSITE; PS0192; T-SNARE; 2.  
KW Synaptosome.  
SQ SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;  
Query Match 100.0%; Score 30; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EEMQRR 6  
DB 12 EEMQRR 17  
RESULT 13  
Q8AXM2 PRELIMINARY; PRT; 206 AA.  
AC Q8AXM2;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE SNAP25a.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
DR EMBL; AF335586; AA013788.1; -.  
DR HSSP; P60881; 1JTH.  
DR GO: GO:0019717; C:synaptosome; IEA.  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR010989; t-snare.  
DR InterPro: IPR000727; T SNARE.  
DR Pfam; PF00835; SNAP-25; 1.  
DR Pfam; PF05739; SNARE; 1.  
DR SMART; SM00397; t-SNARE; 2.  
DR PROSITE; PS0192; T-SNARE; 2.  
KW Synaptosome.  
SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;  
Query Match 100.0%; Score 30; DB 2; Length 206;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6  
Db 12 EEMQRR 17

## RESULT 14

Q640W4 PRELIMINARY; PRT; 206 AA.  
AC Q640W4; 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative";  
RL Dev. Dyn. 225:384-391(2002).  
RN [2]

## SEQUENCE FROM N.A.

RC TISSUE=Eye;  
RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Rahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]

## SEQUENCE FROM N.A.

RC TISSUE=Eye;

RA Klein S., Gerhard D.S.;

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC082475; AAH82475.1; -;

KW Hypothetical protein.

SQ SEQUENCE 206 AA; 23115 MW; 5FF241F6DF2E9C8C CRC64;

Query Match 100.0%; Score 30; DB 2; Length 206;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6  
Db 12 EEMQRR 17

## RESULT 15

Q7Z390

AC Q7Z390 PRELIMINARY; PRT; 216 AA.  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein DKFZp686C04150 (Fragment).  
GN Name=DKFZp686C04150;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

## SEQUENCE FROM N.A.

RC TISSUE=Human colon endothel primary cell culture;  
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Robo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538046; CAD97985.1; -;  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 216 AA; 24473 MW; 68CB647EB074786B CRC64;

Query Match 100.0%; Score 30; DB 2; Length 216;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6  
Db 203 EEMQRR 208

Search completed: February 5, 2005, 23:15:43

Job time : 172 secs

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